



PCT10

**Does Not Comply
Corrected Diskette Needed**

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/019,065

DATE: 07/16/2002
TIME: 13:52:22

Input Set : A:\EP.txt
Output Set: N:\CRF3\07162002\J019065.raw

PatentIn 2.0 "bug". See
p. 7 for explanation

W--> 3 <140> CURRENT APPLICATION NUMBER: US/10/019,065
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3 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

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 804 <213> ORGANISM: human
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 811 20 25 30
 813 Phe Leu Val Thr Lys His Ala Pro Ala Val Ile Thr Cys Thr Ala Ser
 814 35 40 45
 816 Gly Val Pro Phe Pro Ser Ile His Trp Thr Lys Asn Gly Ile Arg Leu
 817 50 55 60
 819 Leu Pro Arg Gly Asp Gly Tyr Arg Ile Leu Ser Ser Gly Ala Ile Glu
 820 65 70 75 80
 822 Ile Leu Ala Thr Gln Leu Asn His Ala Gly Arg Tyr Thr Cys Val Ala
 823 85 90 95
 825 Arg Asn Ala Ala Gly Ser Ala His Arg His Val Thr Leu His Val His
 826 100 105 110
 828 Glu Pro Pro Val Ile Gln Pro Gln Pro Ser Glu Leu His Val Ile Leu
 829 115 120 125
 831 Asn Asn Pro Ile Leu Leu Pro Cys Glu Ala Thr Gly Thr Pro Ser Pro
 832 130 135 140
 834 Phe Ile Thr Trp Gln Lys Glu Gly Ile Asn Val Asn Thr Ser Gly Arg
 835 145 150 155 160
 837 Asn His Ala Val Leu Pro Ser Gly Gly Leu Gln Ile Ser Arg Ala Val
 838 165 170 175
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 841 180 185 190
 843 Thr Ala Leu Gly Lys Ile Lys Leu Asn Val Gln Val Pro Pro Val Ile
 844 195 200 205
 846 Ser Pro His Leu Lys Glu Tyr Val Ile Ala Val Asp Lys Pro Ile Thr
 847 210 215 220
 849 Leu Ser Cys Glu Ala Asp Gly Leu Pro Pro Asp Ile Thr Trp His
 850 225 230 235 240
 852 Lys Asp Gly Arg Ala Ile Val Glu Ser Ile Arg Gln Arg Val Leu Ser

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853	245	250	255
856	Ser Gly Ser Leu Gln Ile Ala Phe Val Gln Pro Gly Asp Ala Gly His		
857	260	265	270
859	Tyr Thr Cys Met Ala Ala Asn Val Ala Gly Ser Ser Ser Thr Ser Thr		
860	275	280	285
862	Lys Leu Thr Val His Val Pro Pro Arg Ile Arg Ser Thr Lys Gly His		
863	290	295	300
865	Tyr Thr Val Asn Glu Asn Ser Gln Ala Ile Leu Pro Cys Val Ala Asp		
866	305	310	315
868	Gly Ile Pro Thr Pro Ala Ile Asn Trp Lys Lys Asp Asn Val Leu Leu		
869	325	330	335
871	Ala Asn Leu Leu Gly Lys Tyr Thr Ala Glu Pro Tyr Gly Glu Leu Ile		
872	340	345	350
874	Leu Glu Asn Val Val Leu Glu Asp Ser Gly Phe Tyr Thr Cys Val Ala		
875	355	360	365
877	Asn Asn Ala Ala Gly Glu Asp Thr His Thr Val Ser Leu Thr Val His		
878	370	375	380
880	Val Leu Pro Thr Phe Thr Glu Leu Pro Gly Asp Val Ser Leu Asn Lys		
881	385	390	395
883	Gly Glu Gln Leu Arg Leu Ser Cys Lys Ala Thr Gly Ile Pro Leu Pro		
884	405	410	415
886	Lys Leu Thr Trp Thr Phe Asn Asn Asn Ile Ile Pro Ala His Phe Asp		
887	420	425	430
889	Ser Val Asn Gly His Ser Glu Leu Val Ile Glu Arg Val Ser Lys Glu		
890	435	440	445
892	Asp Ser Gly Thr Tyr Val Cys Thr Ala Glu Asn Ser Val Gly Phe Val		
893	450	455	460
895	Lys Ala Ile Gly Phe Val Tyr Val Lys Glu Pro Pro Val Phe Lys Gly		
896	465	470	475
898	480		
899	Asp Tyr Pro Ser Asn Trp Ile Glu Pro Leu Gly Gly Asn Ala Ile Leu		
900	485	490	495
901	Asn Cys Glu Val Lys Gly Asp Pro Thr Pro Thr Ile Gln Trp Asn Arg		
902	500	505	510
904	Lys Gly Val Asp Ile Glu Ile Ser His Arg Ile Arg Gln Leu Gly Asn		
905	515	520	525
907	Gly Ser Leu Ala Ile Tyr Gly Thr Val Asn Glu Asp Ala Gly Asp Tyr		
908	530	535	540
910	Thr Cys Val Ala Thr Asn Glu Ala Gly Val Val Glu Arg Ser Met Ser		
911	545	550	555
913	560		
914	Leu Thr Leu Arg Ser Pro Pro Ile Ile Thr Leu Glu Pro Val Glu Thr		
915	565	570	575
916	Val Ile Asn Ala Gly Gly Lys Ile Ile Leu Asn Cys Gln Ala Thr Gly		
917	580	585	590
919	Glu Pro Gln Pro Thr Ile Thr Trp Ser Arg Gln Gly His Ser Ile Ser		
920	595	600	605
922	Trp Asp Asp Arg Val Asn Val Leu Ser Asn Asn Ser Leu Tyr Ile Ala		
923	610	615	620
925	Asp Ala Gln Lys Glu Asp Thr Ser Glu Phe Glu Cys Val Ala Arg Asn		
926	625	630	635
			640

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928 Leu Met Gly Ser Val Leu Val Arg Val Pro Val Ile Val Gln Val His
929 645 650 655
931 Gly Gly Phe Ser Gln Trp Ser Ala Trp Arg Ala Cys Ser Val Thr Cys
932 660 665 670
934 Gly Lys Gly Ile Gln Lys Arg Ser Arg Leu Cys Asn Gln Pro Leu Pro
935 675 680 685
937 Ala Asn Gly Gly Lys Pro Cys Gln Gly Ser Asp Leu Glu Met Arg Asn
938 690 695 700
940 Cys Gln Asn Lys Pro Cys Pro Val Asp Gly Ser Trp Ser Glu Trp Ser
941 705 710 715 720
943 Leu Trp Glu Glu Cys Thr Arg Ser Cys Gly Arg Gly Asn Gln Thr Arg
944 725 730 735
946 Thr Arg Thr Cys Asn Asn Pro Ser Val Gln His Gly Gly Arg Pro Cys
947 740 745 750
949 Glu Gly Asn Ala Val Glu Ile Ile Met Cys Asn Ile Arg Pro Cys Pro
950 755 760 765
952 Val His Gly Ala Trp Ser Ala Trp Gln Pro Trp Gly Thr Cys Ser Glu
953 770 775 780
955 Ser Cys Gly Lys Gly Thr Gln Thr Arg Ala Arg Leu Cys Asn Asn Pro
956 785 790 795 800
958 Pro Pro Ala Phe Gly Gly Ser Tyr Cys Asp Gly Ala Glu Thr Gln Met
959 805 810 815
961 Gln Val Cys Asn Glu Arg Asn Cys Pro Ile His Gly Lys Trp Ala Thr
962 820 825 830
964 Trp Ala Ser Trp Ser Ala Cys Ser Val Ser Cys Gly Gly Ala Arg
965 835 840 845
967 Gln Arg Thr Arg Gly Cys Ser Asp Pro Val Pro Gln Tyr Gly Gly Arg
968 850 855 860
970 Lys Cys Glu Gly Ser Asp Val Gln Ser Asp Phe Cys Asn Ser Asp Pro
971 865 870 875 880
973 Cys Pro Thr His Gly Asn Trp Ser Pro Trp Ser Gly Trp Gly Thr Cys
974 885 890 895
976 Ser Arg Thr Cys Asn Gly Gly Gln Met Arg Arg Tyr Arg Thr Cys Asp
977 900 905 910
979 Asn Pro Pro Pro Ser Asn Gly Gly Arg Ala Cys Gly Gly Pro Asp Ser
980 915 920 925
982 Gln Ile Gln Arg Cys Asn Thr Asp Met Cys Pro Val Asp Gly Ser Trp
983 930 935 940
985 Gly Ser Trp His Ser Trp Ser Gln Cys Ser Ala Ser Cys Gly Gly
986 945 950 955 960
988 Glu Lys Thr Arg Lys Arg Leu Cys Asp His Pro Val Pro Val Lys Gly
989 965 970 975
991 Gly Arg Pro Cys Pro Gly Asp Thr Thr Gln Val Thr Arg Cys Asn Val
992 980 985 990
994 Gln Ala Cys Pro Gly Gly Pro Gln Arg Ala Arg Gly Ser Val Ile Gly
995 995 1000 1005
997 Asn Ile Asn Asp Val Glu Phe Gly Ile Ala Phe Leu Asn Ala Thr Ile
998 1010 1015 1020
1000 Thr Asp Ser Pro Asn Ser Asp Thr Arg Ile Ile Arg Ala Lys Ile Thr

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1003	Asn Val Pro Arg Ser Leu Gly Ser Ala Met Arg Lys Ile Val Ser Ile			
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1006	Leu Asn Pro Ile Tyr Trp Thr Thr Ala Lys Glu Ile Gly Glu Ala Val			
1007		1060	1065	1070
1009	Asn Gly Phe Thr Leu Thr Asn Ala Val Phe Lys Arg Glu Thr Gln Val			
1010		1075	1080	1085
1012	Glu Phe Ala Thr Gly Glu Ile Leu Gln Met Ser His Ile Ala Arg Gly			
1013		1090	1095	1100
1015	Leu Asp Ser Asp Gly Ser Leu Leu Asp Ile Val Val Ser Gly Tyr			
1016		1105	1110	1120
1018	Val Leu Gln Leu Gln Ser Pro Ala Glu Val Thr Val Lys Asp Tyr Thr			
1019		1125	1130	1135
1021	Glu Asp Tyr Ile Gln Thr Gly Pro Gly Gln Leu Tyr Ala Tyr Ser Thr			
1022		1140	1145	1150
1024	Arg Leu Phe Thr Ile Asp Gly Ile Ser Ile Pro Tyr Thr Trp Asn His			
1025		1155	1160	1165
1027	Thr Val Phe Tyr Asp Gln Ala Gln Gly Arg Met Pro Phe Leu Val Glu			
1028		1170	1175	1180
1030	Thr Leu His Ala Ser Ser Val Glu Ser Asp Tyr Asn Gln Ile Glu Glu			
1031		1185	1190	1195
1033	1200			
1034	Thr Leu Gly Phe Lys Ile His Ala Ser Ile Ser Lys Gly Asp Arg Ser			
1036		1205	1210	1215
1037	Asn Gln Cys Pro Ser Gly Phe Thr Leu Asp Ser Val Gly Pro Phe Cys			
1039		1220	1225	1230
1040	Ala Asp Glu Asp Glu Cys Ala Ala Gly Asn Pro Cys Ser His Ser Cys			
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1043	His Asn Ala Met Gly Thr Tyr Cys Ser Cys Pro Lys Gly Leu Thr			
1045		1250	1255	1260
1046	Ile Ala Ala Asp Gly Arg Thr Cys Gln Asp Ile Asp Glu Cys Ala Leu			
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1048	1280			
1049	Gly Arg His Thr Cys His Ala Gly Gln Asp Cys Asp Asn Thr Ile Gly			
1051		1285	1290	1295
1052	Ser Tyr Arg Cys Val Val Arg Cys Gly Ser Gly Phe Arg Arg Thr Ser			
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1069	gcagtaatta cctgcactgc ttccggagtt ccatttcct caattcactg gaccaaaaaat 180			
1070	ggtataagac tgctcccag gggagatggc tatagaattc tgtcctcagg agcaattgaa 240			
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 1075 aaccatgcag ttcttcctag tgccggctta cagatctcca gagctgtccg agaggatgct 540
 1076 ggcacttaca tgttgtggc ccagaacccg gctgtacag ccttggcaa aatcaagtt 600
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 1119 aatgtaccc tcgtatgttgc ttccatgt agaaagatag ttcttattct aaatcccatt 3180
 1120 tattggacaa cagcaaagga aataggagaa gcagtcaatg gctttaccctt caccatgc 3240

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1123 gtcctacagc ttcagtcacc tgctgaagtc actgtaaagg attacacaga ggactacatt 3420
1124 caaacaggtc ctggcagct gtacgcctac tcaaccggc tgttcaccat tgatggcatc 3480
1125 agcatcccat acacatggaa ccacaccgtt ttctatgatc aggcacaggg aagaatgcct 3540
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1127 acactgggtt ttaaaaattca tgottcaata tccaaaggag atcgcaagta tcagtcccc 3660
1128 tccgggttta ccttagactc agttggacct ttttgtgtg atgaggatga atgtgcagca 3720
1129 gggaatccct gctcccatag ctgccacaat gccatggga cttactactg ctccctgcct 3780
1130 aaaggcctca ccatacgctgc agatggaaaga acttgtcaag atattgtatga gtgtgctttg 3840
1131 ggttaggcata cctgccacgc tggtcagac tgtacaata cgattggatc ttatcgctgt 3900
1132 gtggtccgtt gtggaaagtgg ctttcaaga acctctgatg ggctgagttg tcaagatatt 3960
1133 aatgaatgtc aagaatccag ccctgtcacc agcgtgttt caatgccata ggaagttcc 4020
1134 attgtggatg tgaacctggg tatcagctca aaggcagaaa atgcattggat tgt 4073

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/16/2002
PATENT APPLICATION: US/10/019,065 TIME: 13:52:24

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PatentIn 2.0 "bug":

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses(as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/019,065

DATE: 07/16/2002
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Output Set: N:\CRF3\07162002\J019065.raw

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L:1138 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=34
L:0 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (34)